

Figure 1 **Sequence of human APRIL (SEQ ID NOS: 1 and 2)**

Human G70 cDNA (SEQ ID NO 1)

Length: 1465 bp

```

1  GCCAACCTTC CCTCCCCCAA CCCTGGGGCC GCCCCAGGGT TCCTGCGCAC
51  TGCCTGTTCC TCCTGGGTGT CACTGGCAGC CCTGTCCTTC CTAGAGGGAC
101  TGGAACTTAA TTCTCCTGAG GCTGAGGGAG GGTGGAGGGT CTCAAGGCCAA
151  CGCTGGCCCC ACGACGGAGT GCCAGGAGCA CTAACAGTAC CCTTAGCTTG
201  CTTTCCTCCT CCCTCCTTTT TATTTTCAAG TTCTTTTTA TTTCTCCTTG
251  CGTAACAACC TTCTTCCCTT CTGCACCACT GCCCGTACCC TTACCCGCCC
301  CGCCACCTCC TTGCTACCCC ACTCTTGAAA CCACAGCTGT TGGCAGGGTC
351  CCCAGCTCAT GCCAGCCTCA TCTCCTTTCT TGCTAGCCCC CAAAGGGCCT
401  CCAGGCAACA TGGGGGGGCC AGTCAGAGAG CCGGCACTCT CAGTTGCCCT
451  CTGGTTGAGT TGGGGGGCAG CTCTGGGGGC CGTGCTTGT GCCATGGCTC
501  TGCTGACCCA ACAAACAGAG CTGCAGAGCC TCAGGAGAGA GGTGAGCCGG
551  CTGAGGGGGA CAGGAGGCCC CTCCCAGAAT GGGGAAGGGT ATCCCTGGCA
601  GAGTCTCCCG GAGCAGAGTT CCGATGCCCT GGAAGCCTGG GAGAGTGGGG
651  AGAGATCCCG GAAAAGGAGA GCAGTGCTCA CCCAAAAACA GAAGAAGCAG
701  CACTCTGTCC TGCACCTGGT TCCCATTAAAC GCCACCTCCA AGGATGACTC
751  CGATGTGACA GAGGTGATGT GGCAACCAGC TCTTAGGCGT GGGAGAGGCC
801  TACAGGCCCA AGGATATGGT GTCCGAATCC AGGATGCTGG AGTTTATCTG
851  CTGTATAGCC AGGTCCTGTT TCAAGACGTG ACTTTCACCA TGGGTCAAGT
901  GGTGTCTCGA GAAGGCCAAG GAAGGCAGGA GACTCTATTG CGATGTATAA
951  GAAGTATGCC CTCCCACCCG GACCGGGCCT ACAACAGCTG CTATAGCGCA
1001  GGTGTCTTCC ATTTACACCA AGGGGATATT CTGAGTGTC AATTTCCTCG
1051  GGCAAGGGCG AAACCTTAAC TCTCTCCACA TGGAACCTTC CTGGGGTTTG
1101  TGAAACTGTG ATTGTGTTAT AAAAAGTGGC TCCCAGCTTG GAAGACCAGG
1151  GTGGGTACAT ACTGGAGACA GCCAAGAGCT GAGTATATAA AGGAGAGGGA
1201  ATGTGCAGGA ACAGAGGCGT CTTCTGGGT TTGGCTCCCC GTTCCTCACT
1251  TTTCCCTTTT CATTCCCACC CCCTAGACTT TGATTTTACG GATATCTTGC
1301  TTCTGTTCCC CATGGAGCTC CGAATTCTTG CGTGTGTGTA GATGAGGGGC
1351  GGGGGACGGG CGCCAGGCAT TGTTTCAGACC TGGTCGGGGC CCACTGGAAG
1401  CATCCAGAAC AGCACCACCA TCTAACGGCC GCTCGAGGGA AGCACCCGGC
1451  GGTTCGGGCG AAGTC

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The proposed transmembrane domains are boxed

human G70 protein sequence (SEQ ID NO 2)

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1  MPASSPFLLA PKGPPGNMGG PVREPALSVA LWLSWGAALG AVACAMALLT
51  QQTELQSLRR EVSRLQGTGG PSQNGEGYPW QSLPEQSSDA LEAWESGERS
101  RKRRAVLTQK QKKQHSVLHL VPINATSKDD SDVTEVMWQP ALRRGRGLQA
151  QGYGVRIQDA GVYLLYSQVL FQDVTFTMQQ VVSREGQGRQ ETLFRCIRSM
201  PSHPDRAVNS CYSAGVFHLH QGDILSVIIP RARAKLNLSP HGTFLGFVKL

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Figure 2A

Sequence of mouse G70 (SEQ ID NOS: 3 and 4)

Mouse G70 (SEQ ID NO 3)

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1  CATGCCGAGT GCTTTGTGTG TGTTACCTGC TCTAAGAAGC TGGCTGGGCA

51  GCGTTTCACC GCTGTGGAGG ACCAGTATTA CTGCGTGGAT TGCTACAAGA
101 ACTTTGTGGC CAAGAAGTGT GCTGGATGCA AGAACCCCAT CACTGGGTTT
151 GGTAAAGGCT CCAGTGTGGT GGCCTATGAA GGACAATCCT GGCACGACTA
201 CTGCTTCCAC TGCAAAAAAT GCTCCGTGAA TCTGGCCAAC AAGCGCTTTG
251 TATTTCATAA TGAGCAGGTG TATTGCCCTG ACTGTGCCAA AAAGCTGTAA
301 CTTGACGGCT GCCCTGTCTT TCCTAGATAA TGGCACCAA TTCTCCTGAG
351 GCTAGGGGGG AAGGAGTGTC AGAGTGTCAC TAGCTCGACC CTGGGGACAA
401 GGGGGACTAA TAGTACCCTA GCTTGATTTT TTCCTATTCT CAAGTTCTTT
451 TTTATTTCTC CCTTGCGTAA CCCGCTCTTC CCTTCTGTGC CTTTGCCTGT
501 ATTCCCACCC TCCCTGCTAC CTCTTGCCA CCTCACTTCT GAGACCACAG
551 CTGTTGGCAG GGTCCCTAGC TCATGCCAGC CTCATCTCCA GGCCACATGG
601 GGGGCTCAGT CAGAGAGCCA GCCCTTTCGG TTGCTCTTTG GTTGAGTTGG
651 GGGGCAGTTC TGGGGGCTGT GACTTGTGCT GTCGCACTAC TGATCCAACA
701 GACAGAGCTG CAAAGCCTAA GGCGGGAGGT GAGCCGGCTG CAGCGGAGTG
751 GAGGGCCTTC CCAGAAGCAG GGAGAGCGCC CATGGCAGAG CCTCTGGGAG
801 CAGAGTCCTG ATGTCTGGA AGCCTGGAAG GATGGGGCGA AATCTCGGAG
851 AAGGAGAGCA GTACTACCC AGAAGCACAA GAAGAAGCAC TCAGTCTCTG
901 ATCTTGTTCC AGTTAACATT ACCTCCAAGG ACTCTGACGT GACAGAGGTG
951 ATGTGGCAAC CAGTACTTAG GCGTGGGAGA GGCCTGGAGG CCCAGGGAGA
1001 CATTGTACGA GTCTGGGACA CTGGAATTTA TCTGCTCTAT AGTCAGGTCC
1051 TGTTTCATGA TGTGACTTTC ACAATGGGTC AGGTGGTATC TCGGGAAGGA
1101 CAAGGGAGAA GAGAACTCT ATTCCGATGT ATCAGAAGTA TGCCTTCTGA
1151 TCCTGACCGT GCCTACAATA GCTGCTACAG TGCAGGTGTC TTTCAATTTAC
1201 ATCAAGGGGA TATTATCACT GTCAAAATTC CACGGGCAA CGCAAACTT
1251 AGCCTTTCTC CGCATGGAAC ATTCCTGGGG TTTGTGAAAC TATGATTGTT
1301 ATAAAGGGGG TGGGGATTTT CCAATCCAAA AACTGGCTAG ACAAAGGACA
1351 AGGAACGGTC AAGAACAGCT CTCCATGGCT TTGCCTTGAC TGTTGTTTCT
1401 CCCTTTGCCT TTCCCGCTCC CACTATCTGG GCTTTGACTC CATGGATATT
1451 AAAAAAGTAG AATATTTTGT GTTTATCTCC CAAAAA
  
```

09855158.051404

Figure 2B

Mouse G70 Length: 241 (SEQ ID NO 4)

```
1  MPASSPGHMG GSVREPALSV ALWLSWGAVL GAVTCAVALL IQQTELQSLR
51  REVSRLQRSG GPSQKQGERP WQSLWEQSPD VLEAWKDGA SRRRRAVLTO
101 KHKKKHSQLH EVPVNITSKD SDVTEVMWQP VLRRGRGLEA QGDIVRVWDT
151 GIYLLYSQVL FHDVTFTMGQ VVSREGQGR ETLFRCIRSM PSDPDRAVNS
201 CYSAGVFHLH QGDIITVKIP RANAKLSLSP HGTFLGFVKL *
```

G-70 FLAG des92 (smuG70) Strain #4081 (SEQ ID NO 19):

```
MDYKDDDDKKHKKKHSVLHLPVNITSKSDVTEVMWQPVLRGRGLEAQGDIVRVW
DTGIYLLYSQVLFHDVTFTMGQVVSREGQGRRETLFRCIRSMPSDPDRAYNSCYSAG
VFHLHQGDIITVKIPRANAKLSLSPHGTFLGFVKL*
```

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Figure 3
Alignm. of human and mouse G70

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mouse: 1  MPASS-----PGHMGGSVREPALSVALWLSWGAVLGAVTCAVALLIQQTEQLSLRR 51
          MPASS          PG+MGG VREPALSVALWLSWGA LGAV CA+ALL QQTEQLSLRR
Human: 1  MPASSPFLAPKGPFGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTEQLSLRR 60

mouse: 52  EVSRLQRSGGPSQKQGERPWQSLWEQSPDVLEAWKDGAKSRRRRRAVLTKHKKKHSVLHL 111
          EVSRLQ +GGPSQ      PWQSL EQS D LEAW+ G +SR+RRRAVLTKK+HSLHL
human: 61  EVSRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWESGERSRKRRRAVLTKKQKKHSLHL 120

mouse: 112 VPVNITSKD-SDVTEVMWQPVLRRGRGLEAQGDIVRVWDTGIYLLYSQVLFHDVFTTMGQ 170
          VP+N TSKD SDVTEVMWQP LRRGRGL+AQG VR+ D G+YLLYSQVLF DVTFTTMGQ
human: 121 VPINATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTTMGQ 180

mouse: 171 VVSREGQGRRETLFRCIRSMPSDPDRAYNSCYSAGVFHLHQGDIITVKIPRANAKLSLSP 230
          VVSREGQGR+ETLFRCIRSMPS PDRAYNSCYSAGVFHLHQGDI++V IPRA AKL+LSP
human: 181 VVSREGQGRQETLFRCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRRAKLNLSLSP 240

mouse: 231 HGTFGLGFVKL 240
          HGTFGLGFVKL
human: 241 HGTFGLGFVKL 250

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Fig. 4A

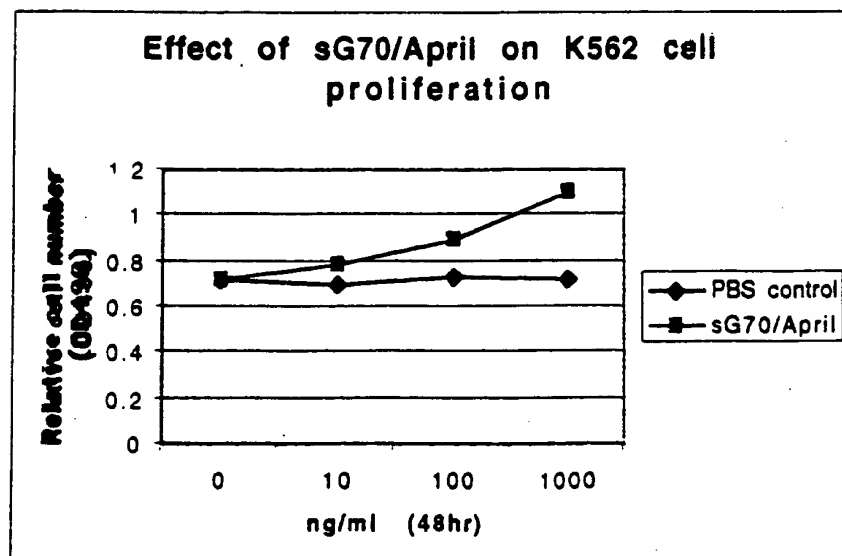
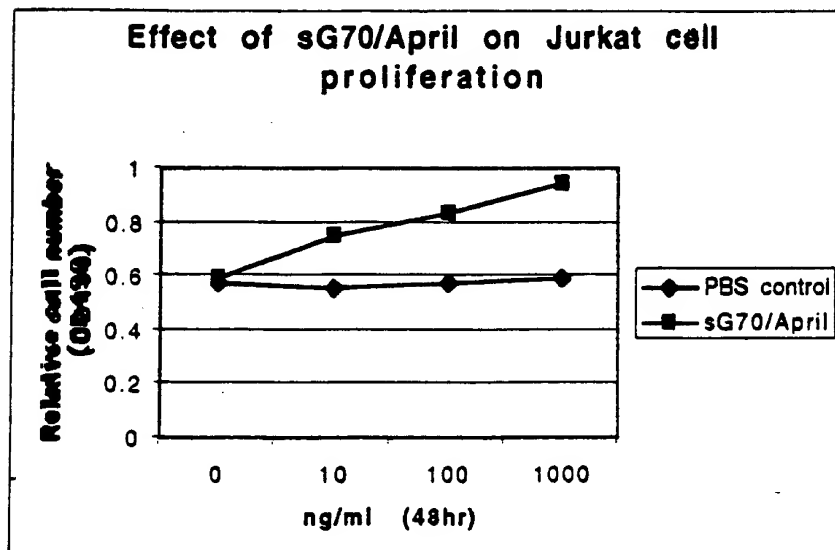
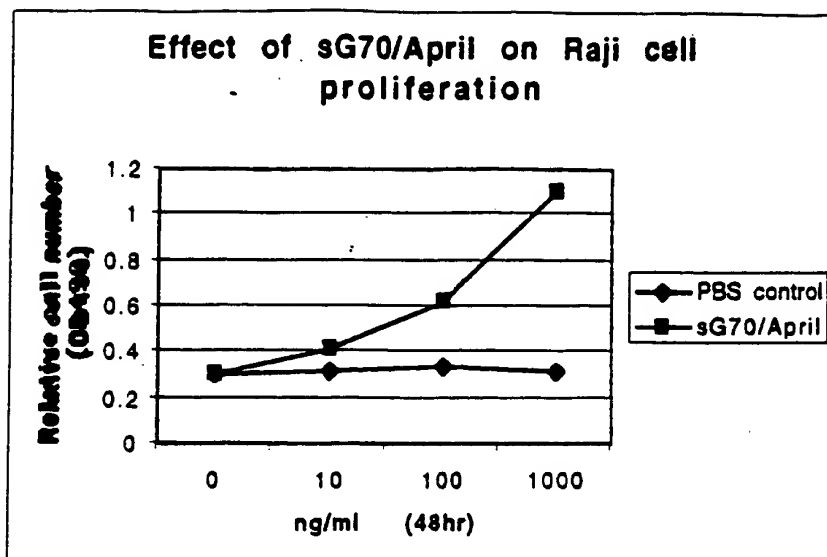


Fig. 4B

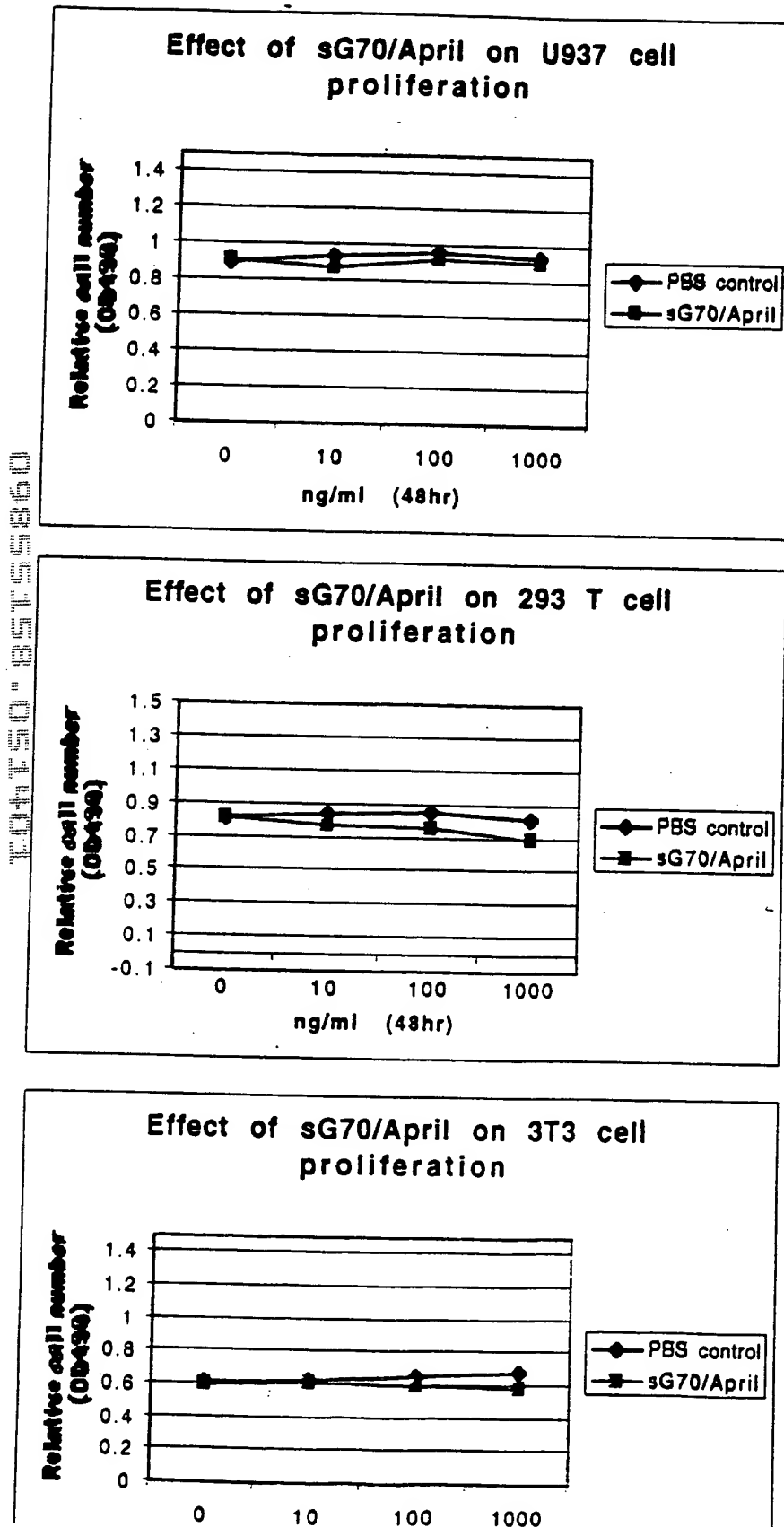
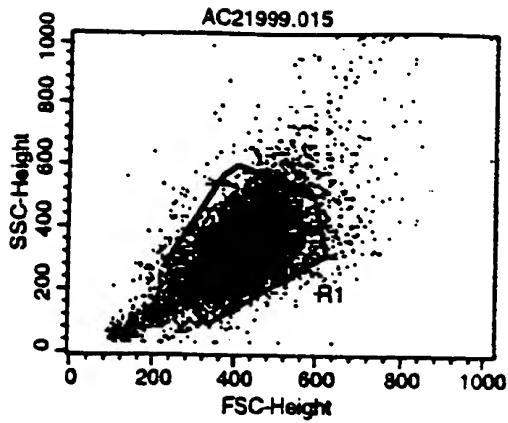


FIGURE 5A



FACS analysis of G70/April receptor binding

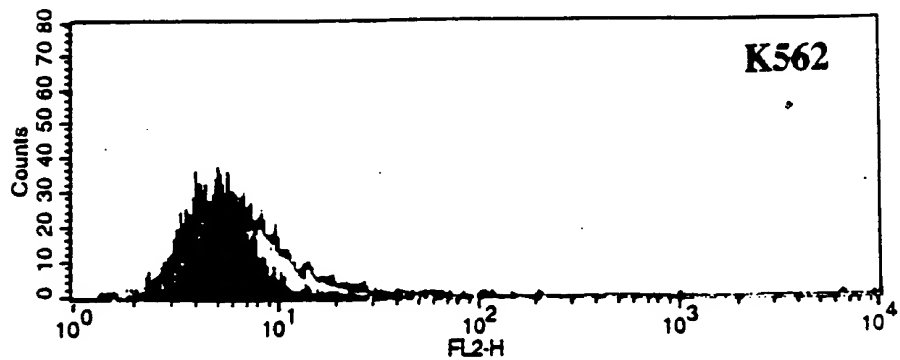
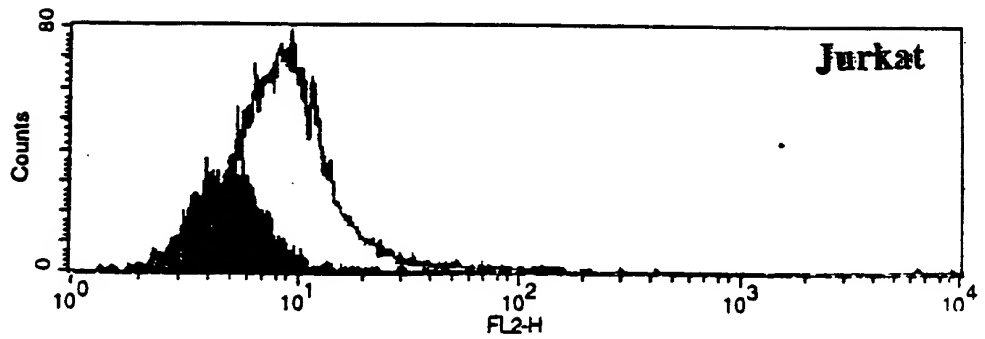
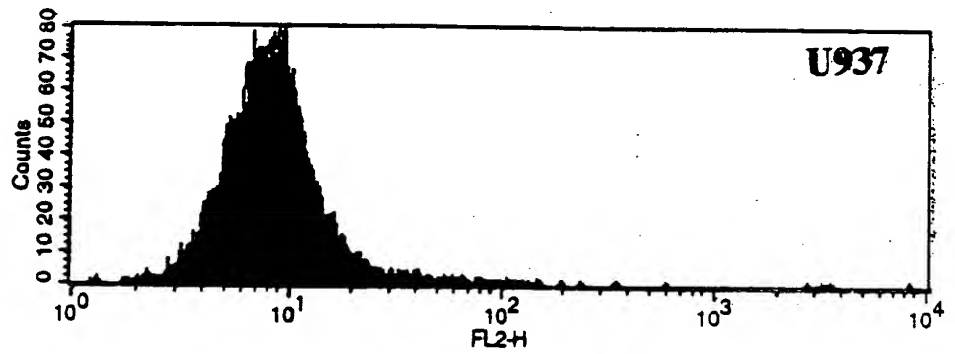
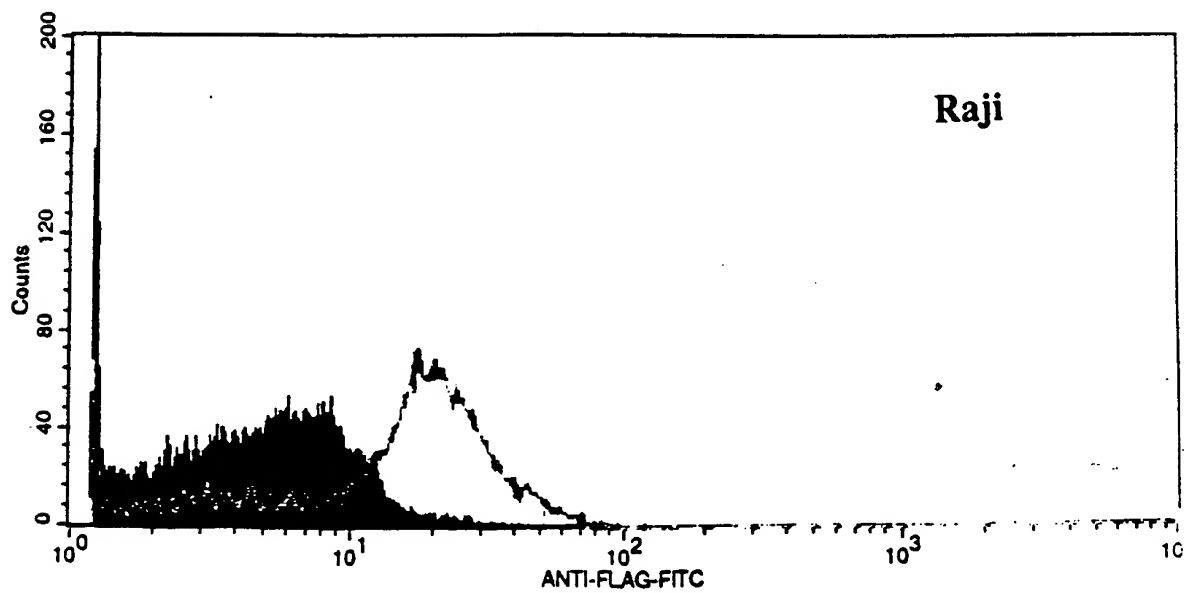
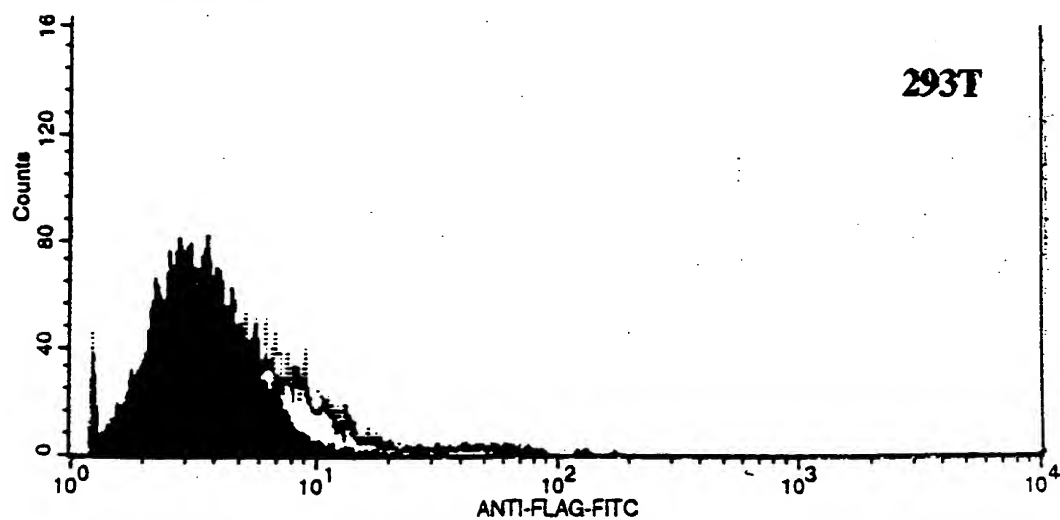
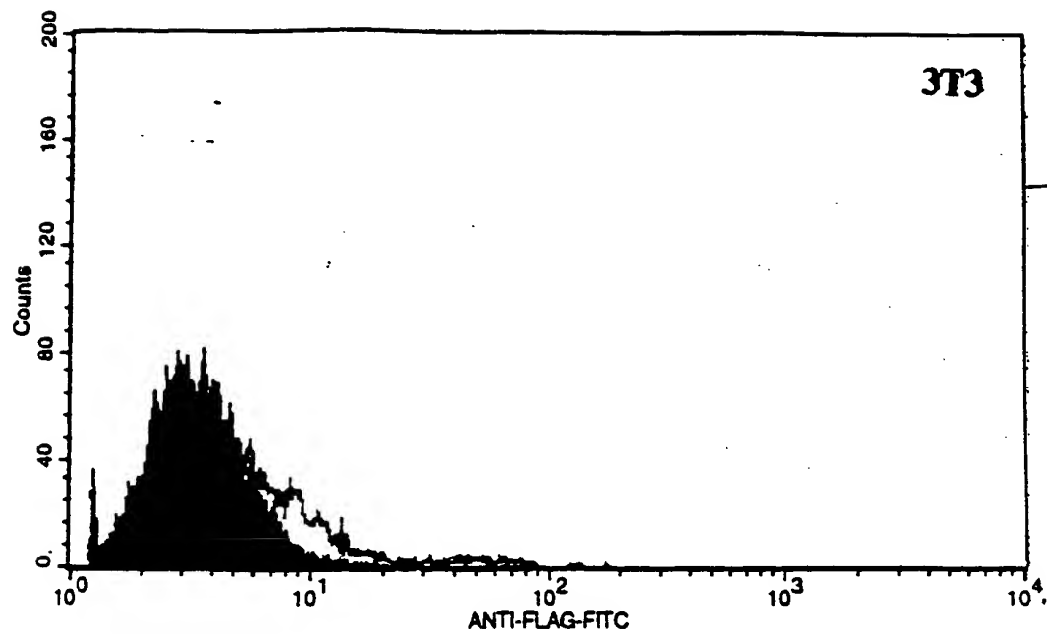
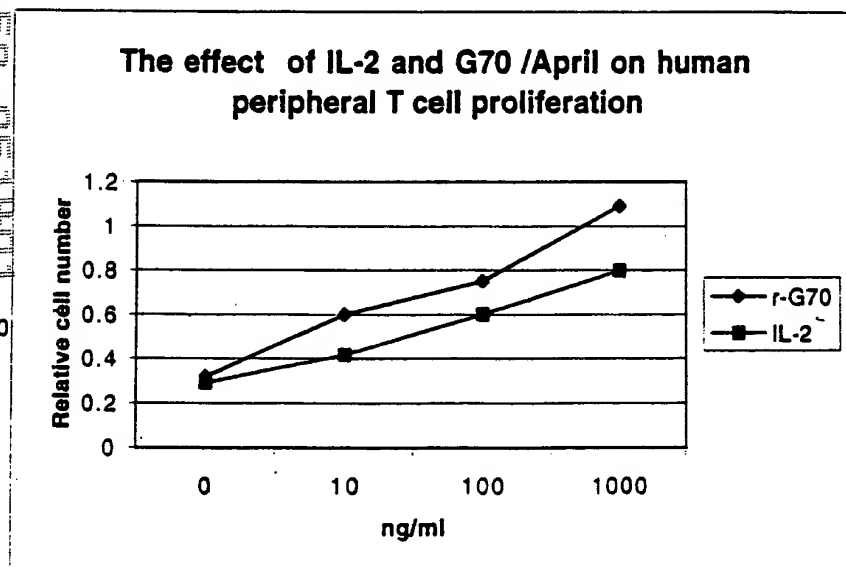
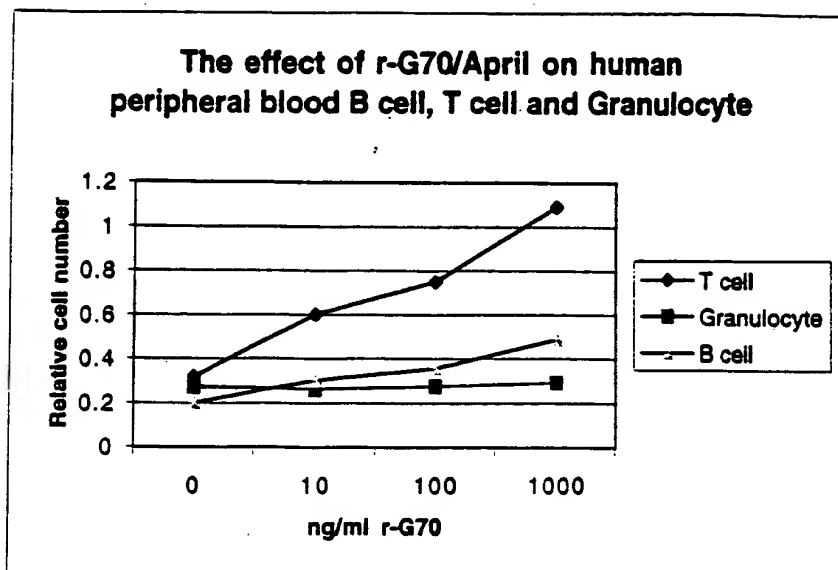


FIGURE 5B



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Fig. 7

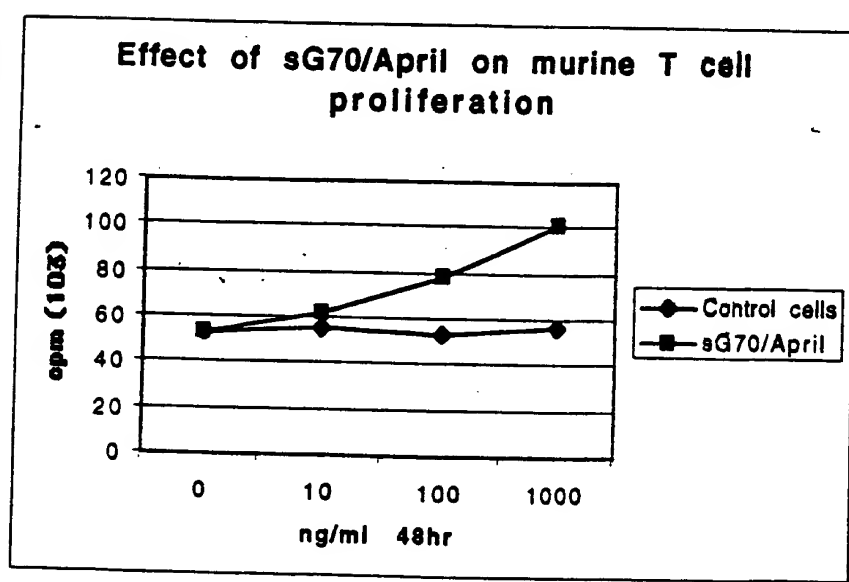
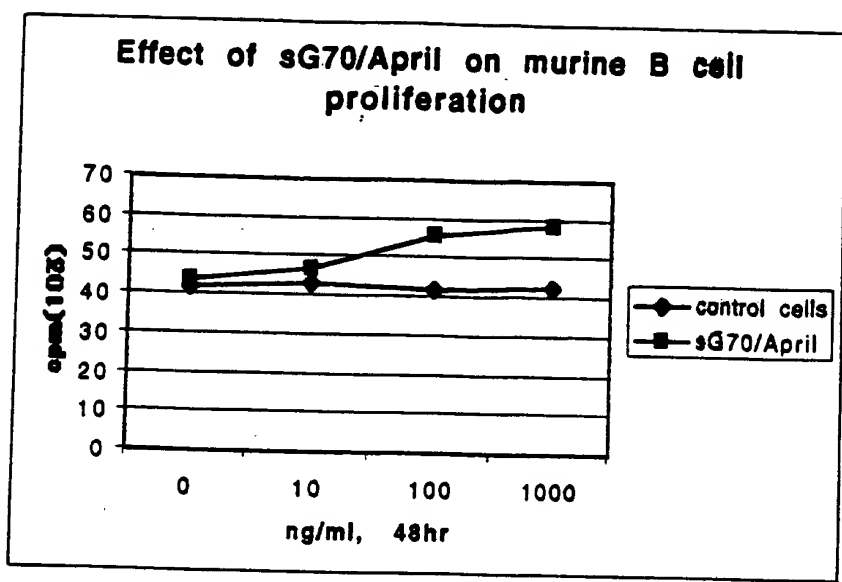


Fig. 8

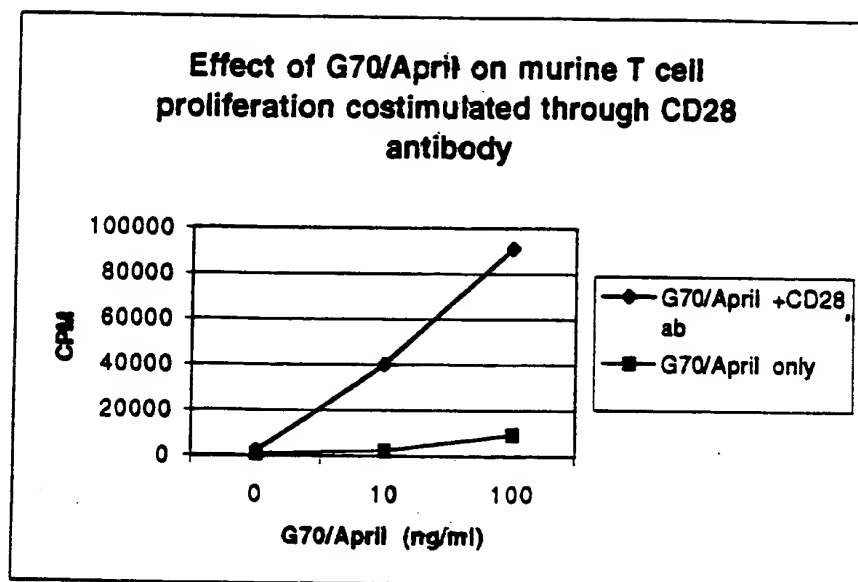


Fig. 9

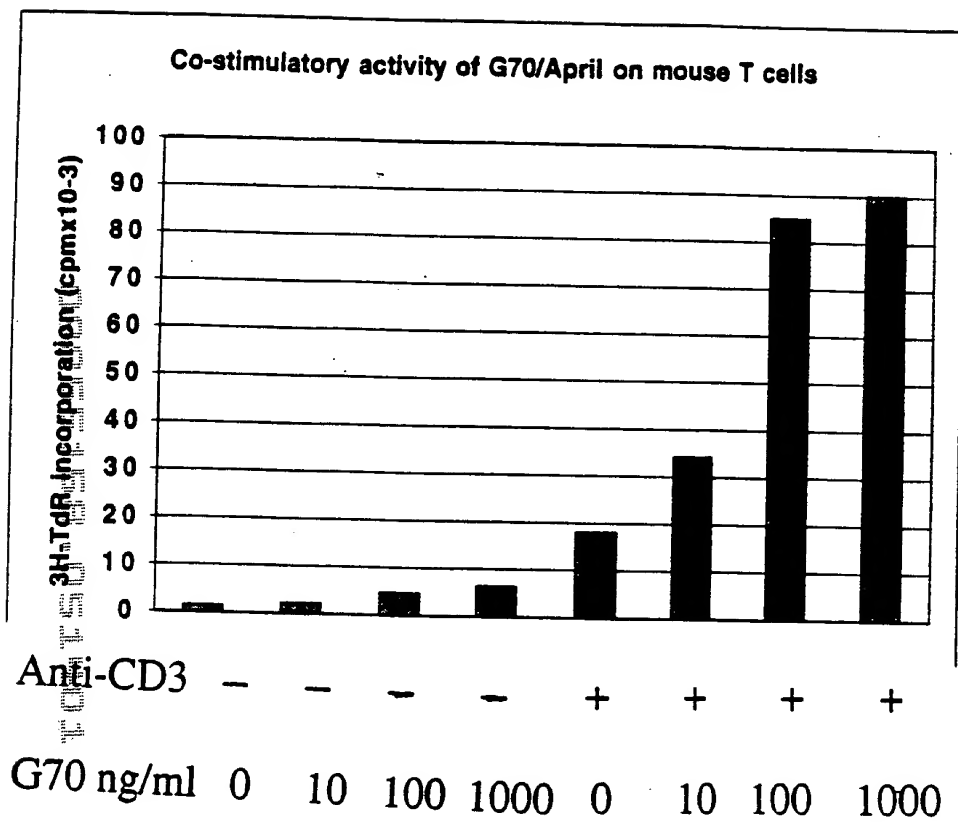


Figure 10A
Human BCMA

Human (SEQ ID NO: 5):

1 MAGQCSQNEY FDSLLHACIP CQLRCSSNTP PLTCQRYCNA
SVTNSVKGTN

51 AILWTCLGLS LIISLAVFVL MFLLRKISSE PLKDEFKNTG
SGLLGMANID

101 LEKSRTGDEI ILPRGLEYTV EECTCEDCIK SKPKVDSDDHC
FPLPAMEEGA

151 TILVTTKTND YCKSLPAALS ATEIEKSISA R

Human (SEQ ID NO: 5):

MAGQCSQ NEYFDSLLHA CIPCQLRCSS NTPPLTCQRY CNASVTNSVK
GTNA ILWTCL GLSLIISLAV FVLMFLLRKI SSEPLKDEFK NTGSGLLGMA
NIDLEKSRTG DEILPRGLE YTVEECTCED CIKSKPKVDS DHCFLPAME
EGATILVTTK TNDYCKSLPA ALSATEIEKS ISAR

hBCMA's extracellular domain (SEQ ID NO: 6):

MAGQCSQ NEYFDSLLHA CIPCQLRCSS NTPPLTCQRY CNASVTNSVK
GTNA

hBCMA's cysteine-rich consensus region (SEQ ID NO: 7):

CSQ NEYFDSLLHA CIPCQLRCSS NTPPLTCQRY C

hBCMA's transmembrane region (SEQ ID NO: 8):

ILWTCL GLSLIISLAV FVLMF

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Figure 10B

huBCMA-Fc (SEQ ID NO: 9):

MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNA
GGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGK*

muBCMA-Fc (SEQ ID NO: 10):

MAQQCFHSEYFDSLLHACKPCHLRCSNPPATCQPYCDPSVTSSVKGSYTG
GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGK*

0955153-051401

Figure 11 **Alignment of human BCMA amino acid sequence and** **murine BCMA amino acid sequence**

murine BCMA amino acid sequence Length: 185 (SEQ ID NO: 11):

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1  MAQQCFHSEY FDSLLHACKP CHLRCSNPPA TCQPYCDPSV TSSVKGTYTV
51 LWIFLGLTLV LSLALFTISF LLRKMNPEAL KDEPQSPGQL DGSAQLDKAD
101 TELTRIRAGD DRIFPRSLEY TVEECTCEDC VKSKPKGDS D HFFPLPAMEE
151 GATILVTTKT GDYKSSVPT ALQSVGMMEK PTHTR

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alignment of human BCMA amino acid sequence and murine BCMA amino acid sequence.

```

Query:      4  MAGQCSQNEYFDSLLHACIPCQLRCSNTPLTCQRYCNASVTNSVKGTNAILWTCGLS 63
             MA QC  +EYFDSLLHAC PC LRCS+  PP TCQ YC+ SVT+SVKGT  +LW  LGL+
Sbjct:      1  MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT 58

Query:     64  LIISLAVFVLMFLLRKISSEPLKDEFKNTG----SGLLGMANIDLEKSR TGDEIILPRGL 119
             L++SLA+F + FLLRK++ E LKDE ++ G   S  L  A+ +L + R GD+ I PR L
Sbjct:     59  LVL LSLALFTISFLLRKMNPEALKDEPQSPGQLDGSAQLDKADTELTRIRAGDDRIFPRSL 118

Query:    120  EYTVVEECTCEDCIKSKPKVDS DHCFPLPAMEEGATILVTTKTNDYCKS-LPAAL-SATEI 177
             EYTVVEECTCEDC+KSKPK DSDH FPLPAMEEGATILVTTKT DY KS +P AL S   +
Sbjct:    119  EYTVVEECTCEDCVKSKPKGDS DHFFPLPAMEEGATILVTTKTGDYKSSVPTALQSVGMGM 178

Query:     178  EKSISAR 184
             EK   R
Sbjct:     179  EKPTHTR 185

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Figure 12A
Human TACI

huTACI (SEQ ID NO: 14).

1 MSGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCMSC
51 KTICNHQSQR TCAAFCRSLs CRKEQGKFYD HLLRDCISCA SICGQHPKQC
101 AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL
151 PGLKLSADQV ALVYSTLGLC LCAVLCCFLV AVACFLKKRG DPCSCQPRSR
201 PRQSPAKSSQ DHAMEAGSPV STSPEPVETC SFCFPECRAP TQESAVTPGT
251 PDPTCAGRWG CHTRTTVLQP CPHIPDSGLG IVCVPAQEGG PGA

MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSC
KTICNHQSQR TCAAFCRSLs CRKEQGKFYD HLLRDCISCA SICGQHPKQC
AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL
PGLKLSADQV ALVYSTLGLC LCAVLCCFLV AVACFLKKRG DPCSCQPRSR
PRQSPAKSSQ DHAMEAGSPV STSPEPVETC SFCFPECRAP TQESAVTPGT
PDPTCAGRWG CHTRTTVLQP CPHIPDSGLG IVCVPAQEGG PGA

huTACI's extracellular domain (SEQ ID NO: 15):

1 MSGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCMSC
51 KTICNHQSQR TCAAFCRSLs CRKEQGKFYD HLLRDCISCA SICGQHPKQC
101 AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL
151 PGLKLSADQV ALVYST

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Figure 12B

huTACI's cysteine-rich consensus region (SEQ ID NO: 16):

CPEEQYWDPLLGTCSCKTICNHQSQR TCAAF C and
CRKEQGKFYDHLLRDCISCASICGQHPKQCA YFC

transmembrane region (SEQ ID NO: 17):

LGLCLCAVLCCFLVAVACFL

hTACI-Fc (SEQ ID NO: 18):

1 MSGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCSMC

51 KTICNHQSQR TCAAFCRSL S CRKEQGKFYD HLLRDCISCA SICGQHPKQC

101 AYFCENKLRS PVNLPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL

151 PGLKLSADQV ALVYSGGGGG DKHTCPCP APPELLGGPSV FLFPKPKDT

201 LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY

251 RVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT

301 LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS

351 DGSFFLYSKL TVDKSRWQQG NVFSCSV MHE ALHNHYTQKS LSLSPGK*

095513-0544

Figure 13

Alignment of cysteine rich extracellular regions of human TACI and human BCMA.

```
34 CPEEQYWDPLLGTCSCKTICNHQS.QRTCAAFCSRSLSCRKEQGKFYDHL 82
   | : : | . | | | . | . | . | . | | : | . | . :
8  CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT..NAI 55

      83 LRDCISCASI 92
      | | : . |
56 LWTCLGLSLI 65
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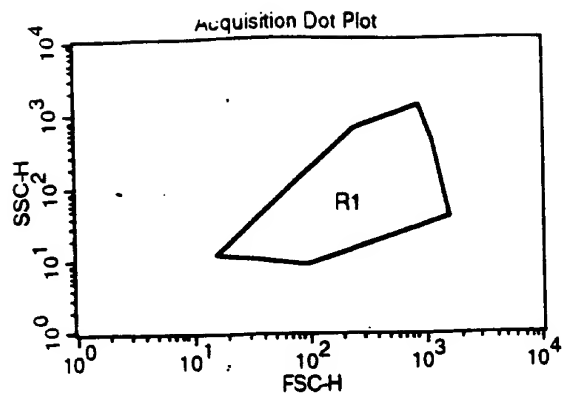
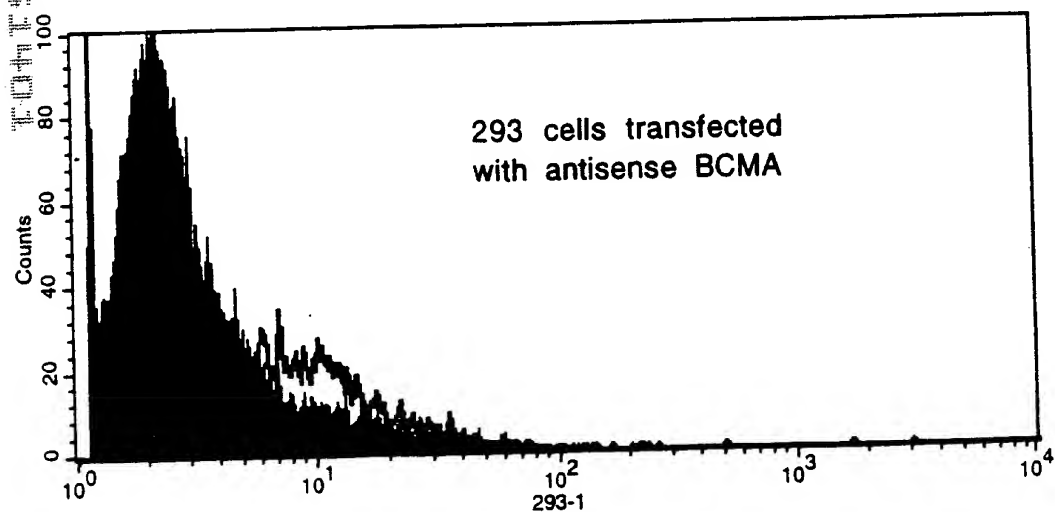
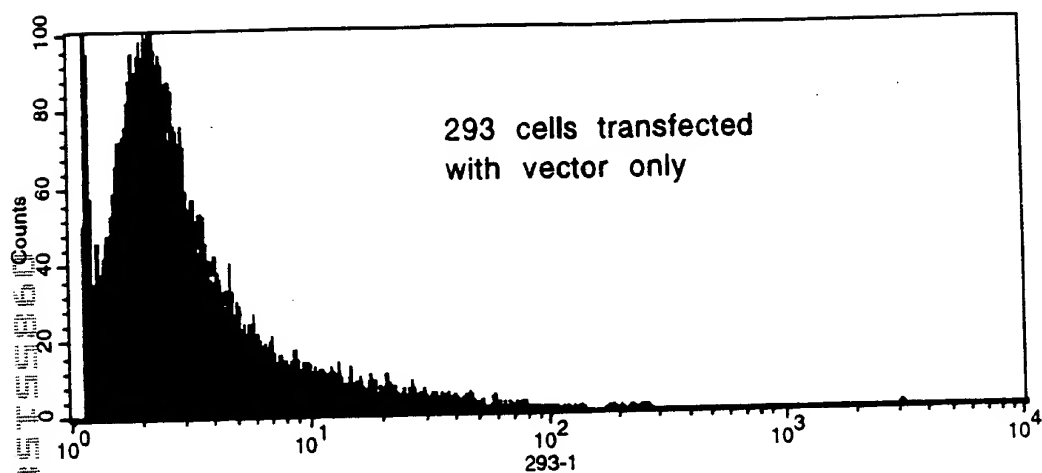


Fig.14



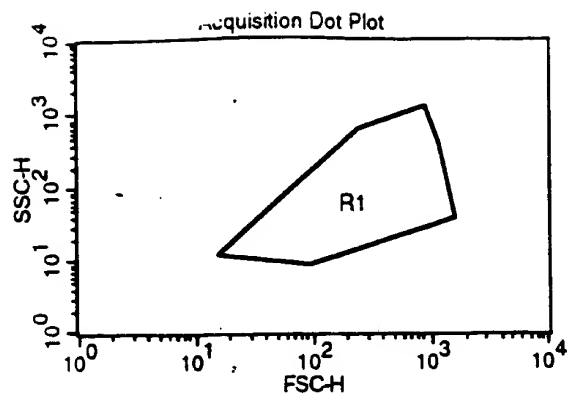
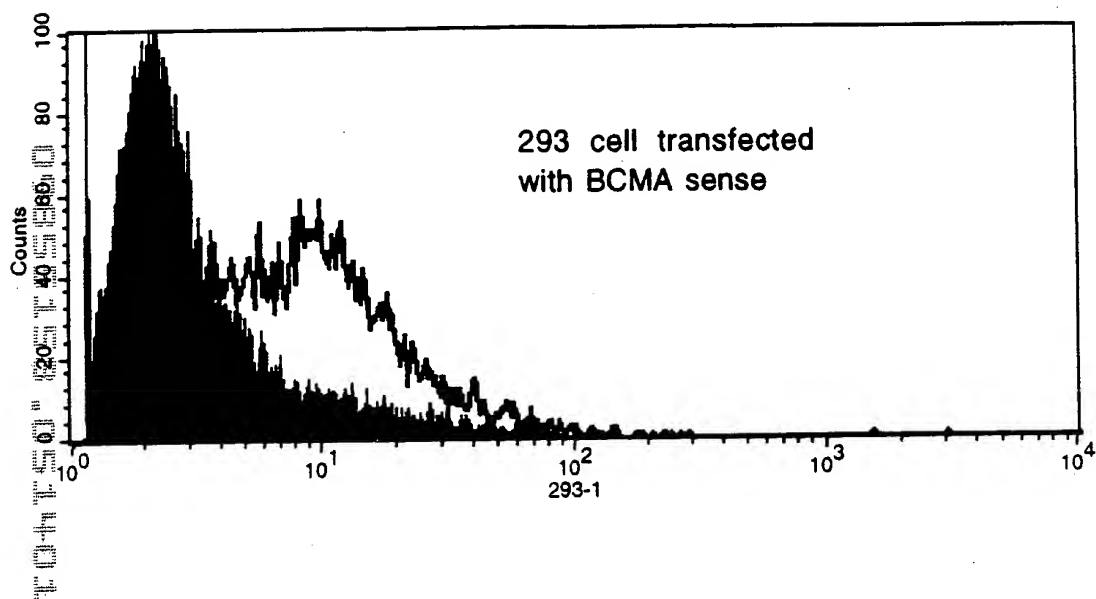


Fig.14



C.

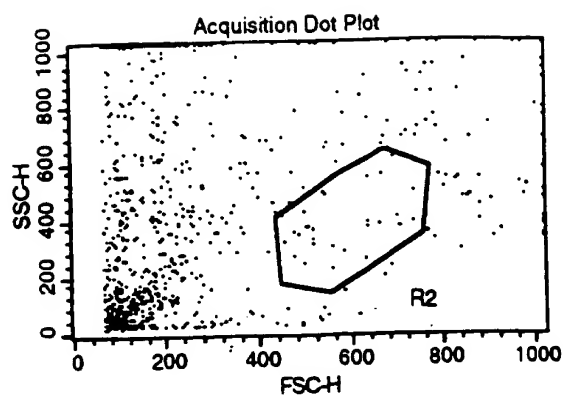
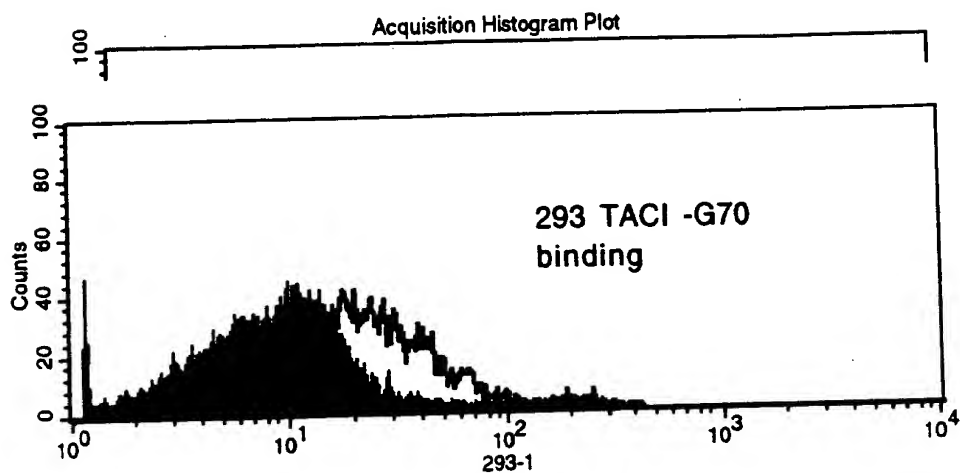
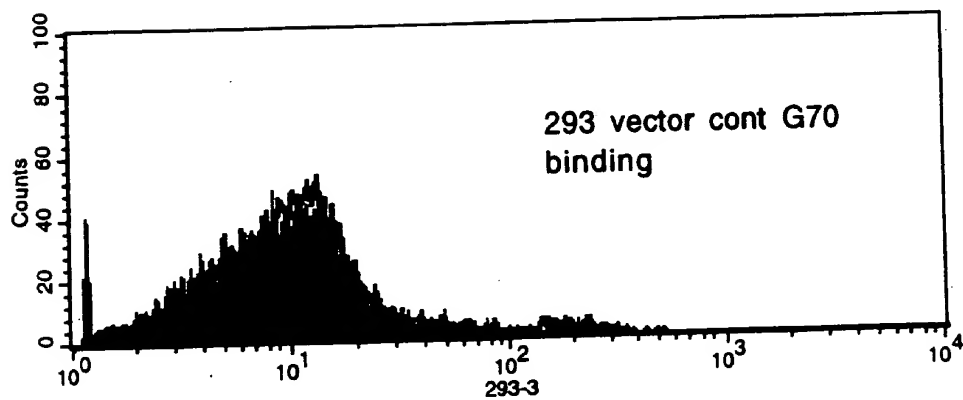


Fig. 15



A.



B.

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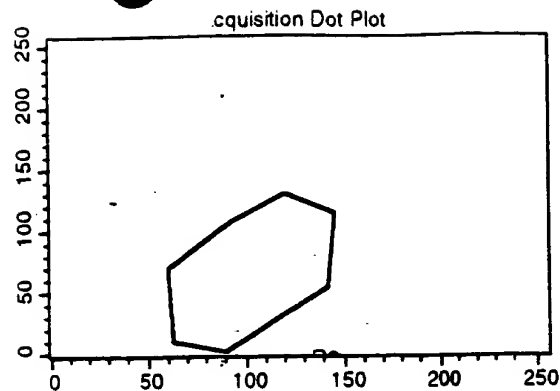
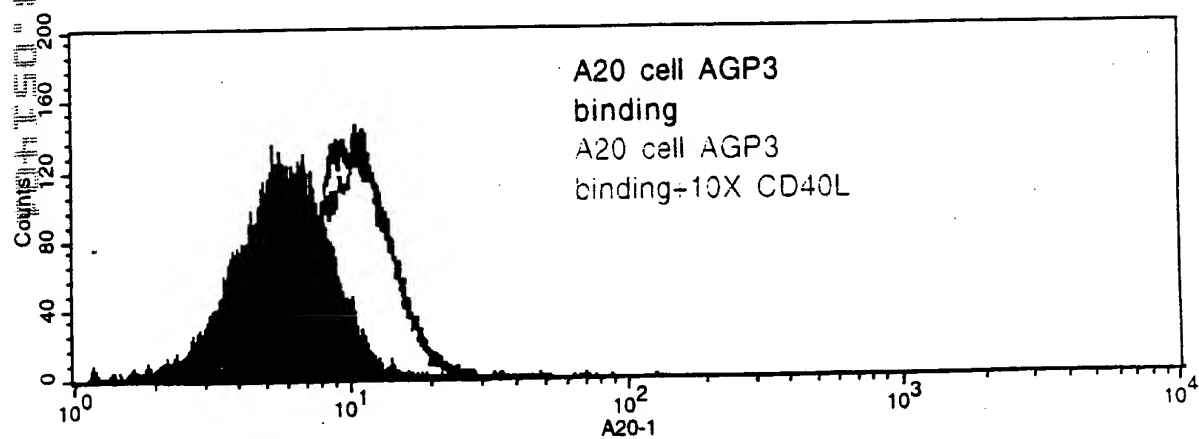
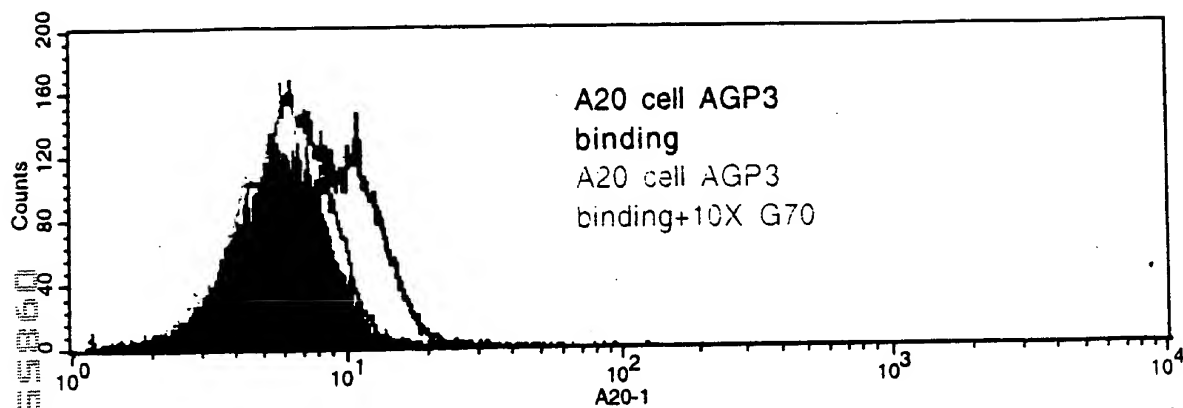


Fig. 16



Experiment 4-3-2000

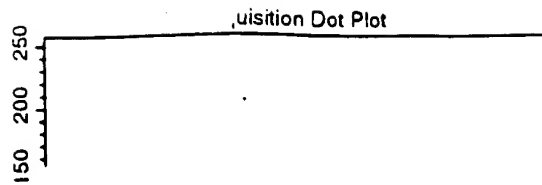
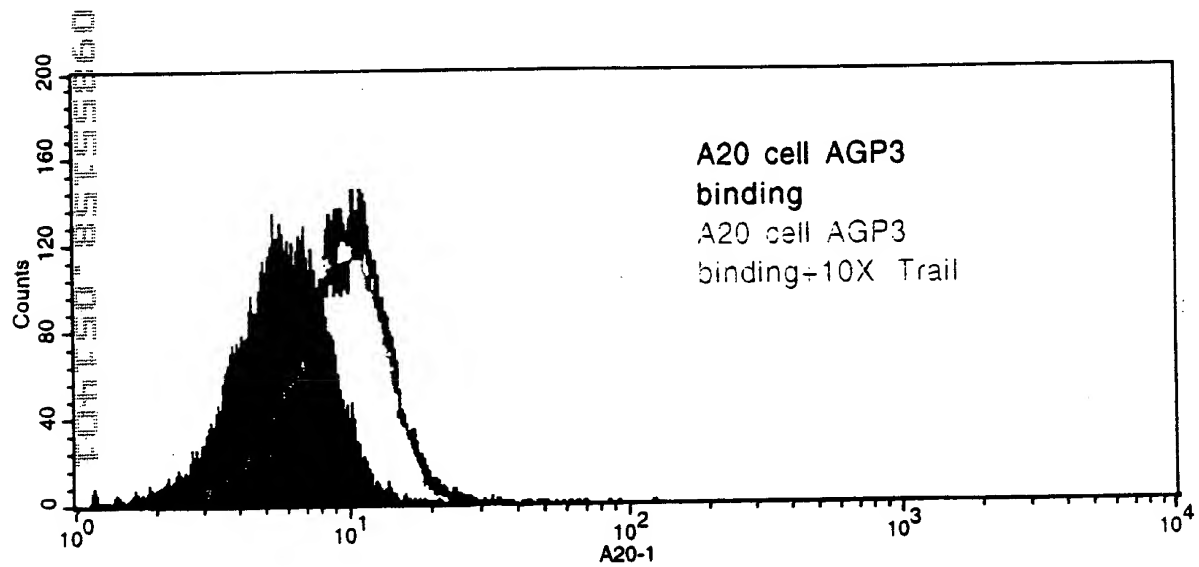
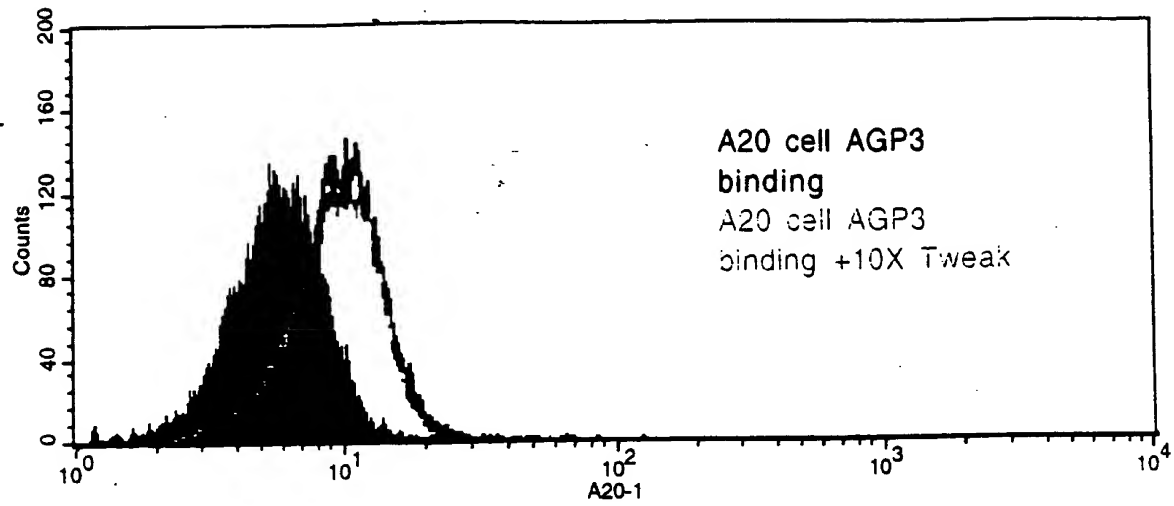
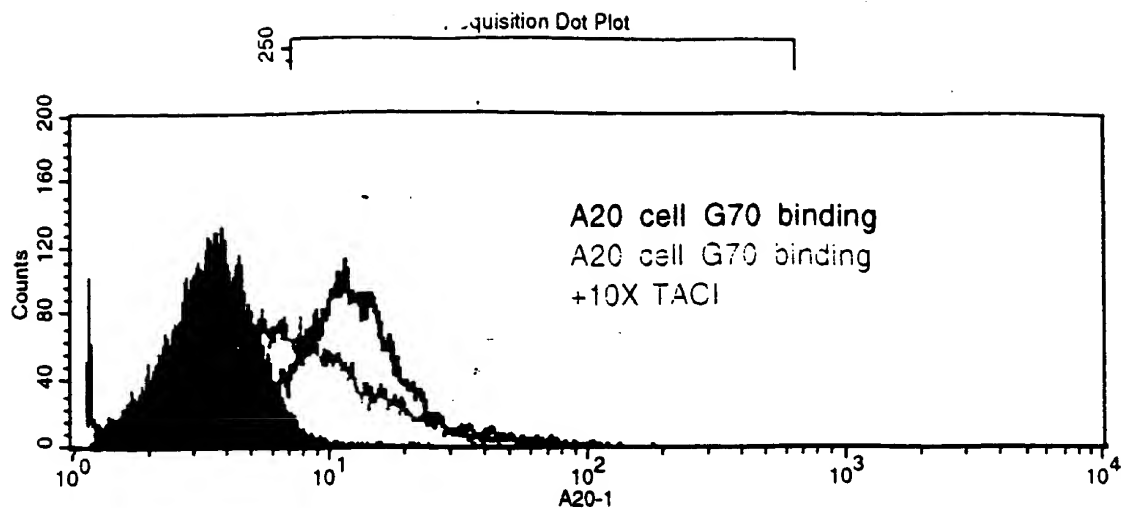


Fig. 16

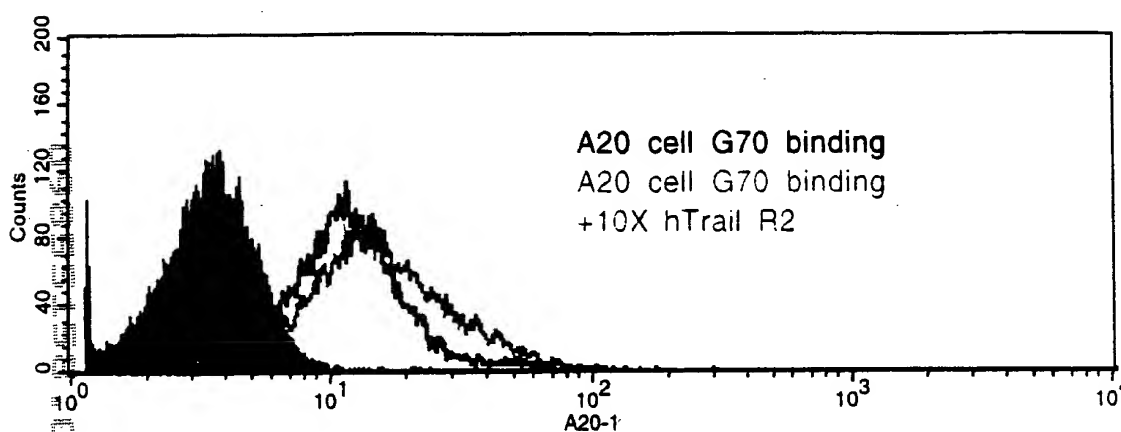


Experiment 4-3-2000

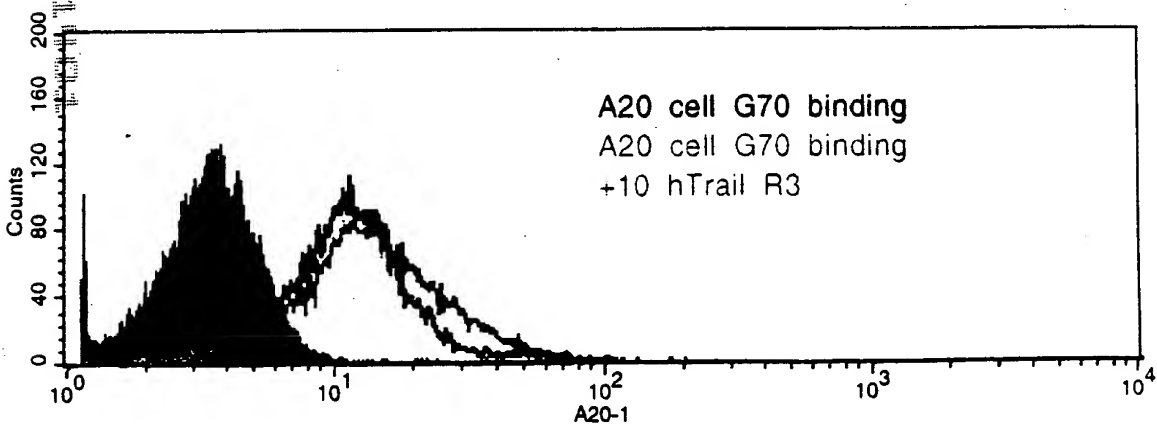
Fig.17



A.



B.



C.

Experiment
4-11-2000

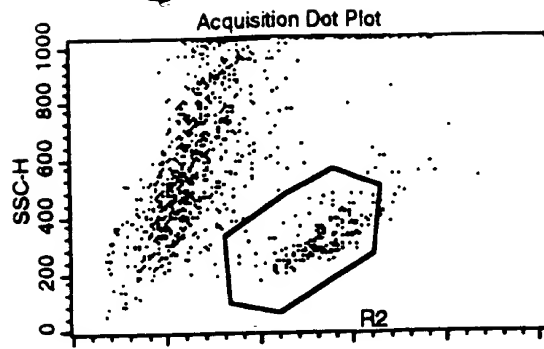
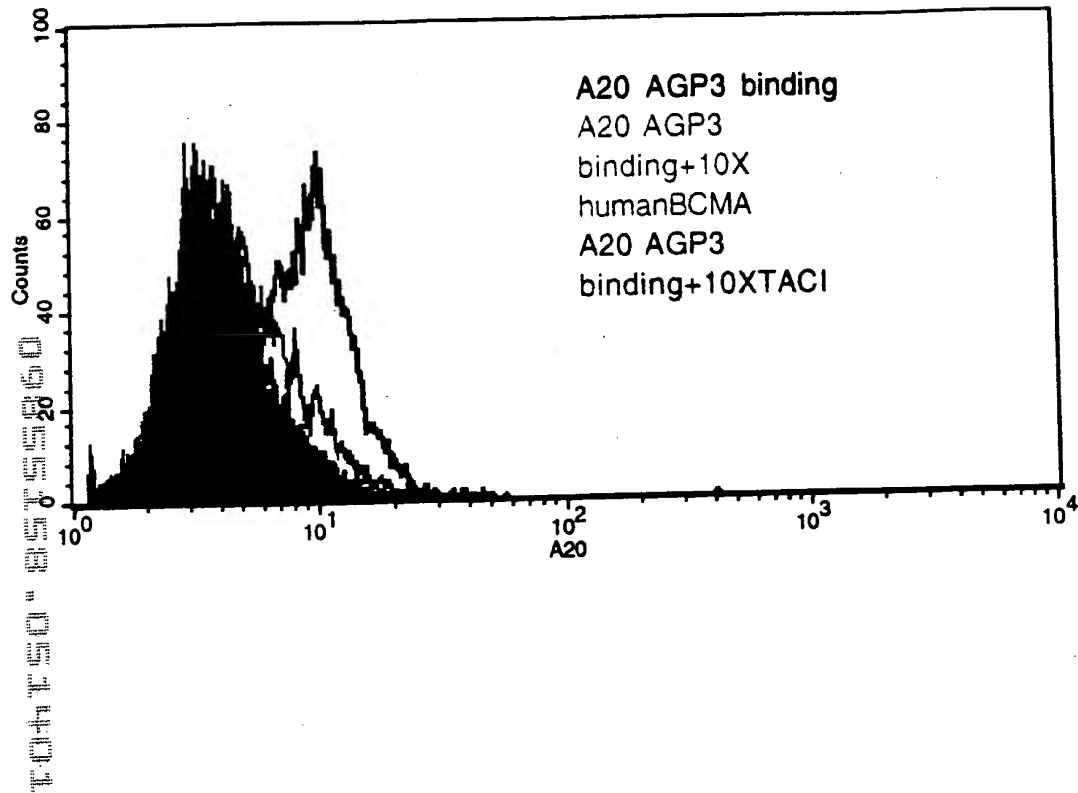


Fig.18



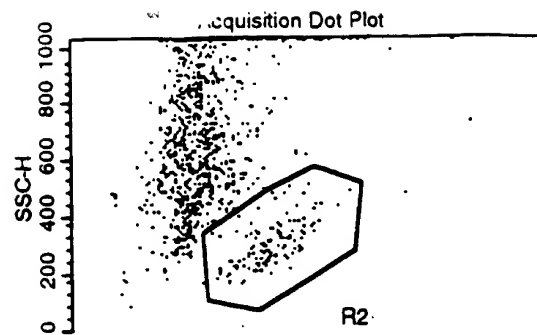
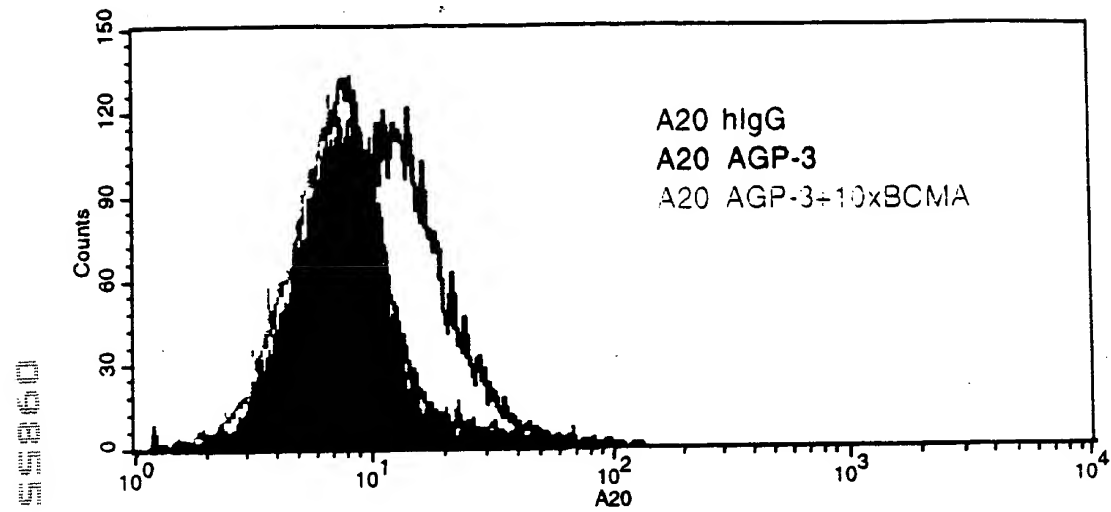
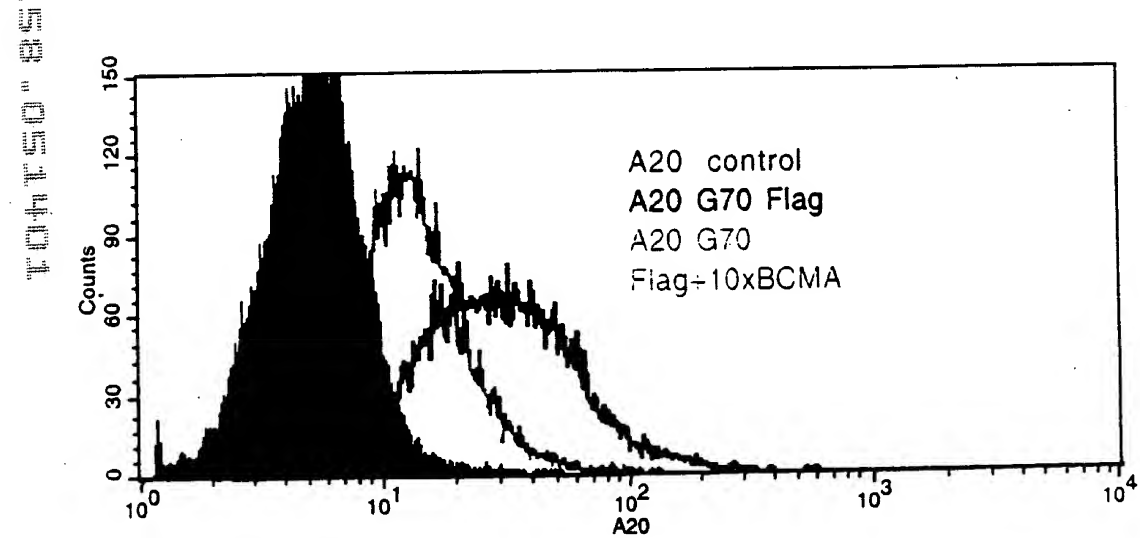


Fig.19

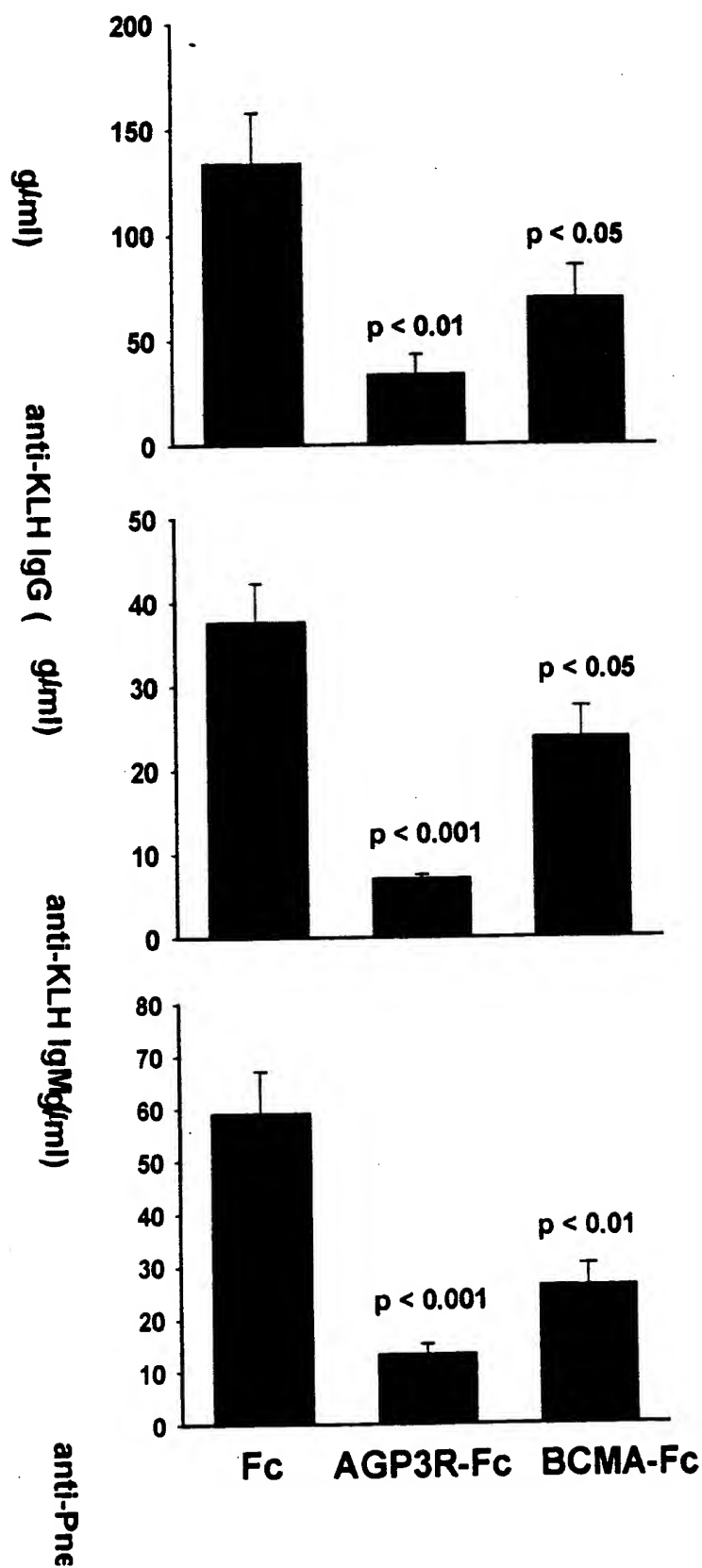


A.



B.

Fig.20



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